

## AMENDMENTS TO THE CLAIMS:

The following listing of claims will replace all prior versions and listings of claims in the application.

1-16. (Cancelled)

17. (Currently amended) A method of simultaneously detecting or quantifying  $n$  kinds of different target nucleic acids in a specimen, wherein each target nucleic acid contains a first predetermined partial sequence Fa and a second predetermined partial sequence Sa and the nucleic acid is set forth as (Fa, Sa) each having a predetermined first partial sequence Fa and a predetermined second partial sequence Sa, wherein Fa is any one of the first predetermined partial sequences F1 to F $n$ , ~~wherein  $n$  is an integer of 2 or more;~~ and Sa is any one of the second predetermined partial sequences S1 to S $n$ , wherein  $n$  is an integer of 2 or more ~~in a specimen~~ comprising:

(a) preparing probes Aa and Ba, wherein Aa is any one of the probe groups A1 to A $n$  and ~~wherein  $n$  is an integer of 2 or more~~ and Ba is any one of the probe groups B1 to B $n$ , ~~and wherein  $n$  is an integer of 2 or more,~~

said ~~probes~~ probe Aa being one of the respective first probes each of which has a sequence F'a complementary to the respective first partial sequence Fa of the target nucleic acid (Fa, Sa) and a first binding molecule bound to the sequence F'a, wherein F'a is any one of the sequences F'1 to F' $n$  and wherein  $n$  is an integer of 2 or more, and

said ~~probes~~ probe Ba being one of the respective second probes each of which has a sequence S'a complementary to the respective second partial sequence Sa of the target nucleic acid and a flag bound to the sequence S'a, wherein said flag comprises four units SD, D0 $_j$ , D1 $_k$ , and ED, each having a desired sequence, and linked in the form of SD+ D0 $_j$ + D1 $_k$ + ED; wherein the flag sequences D0 $_j$  and D1 $_k$  are located between SD and ED and a combination of the D0 $_j$  and D1 $_k$  as set forth in (D0 $_j$ , D1 $_k$ ) being assigned respectively to the each of the respective target nucleic ~~acids~~acid (Fa, Sa); and wherein SD and ED are each primer sequences, wherein S'a is any one of the sequences S'1 to S' $n$  and wherein  $n$  is an integer of 2 or more, and wherein  $j$  and  $k$  are arbitrary natural numbers,

(b) mixing ~~each pair of the probes~~ probe Aa and ~~the probes~~ probe Ba with specimens containing target nucleic ~~acids~~acid (Fa, Sa), respectively, thereby hybridizing the first ~~probes~~ probe Aa with the respective first partial ~~sequences~~sequence Fa of the target nucleic ~~acids~~acid and simultaneously hybridizing the second ~~probes~~ probe Ba with the respective second partial sequence Sa of the target nucleic ~~acids~~acid;

(c) ligating the first ~~probes~~ probe Aa and the second ~~probes~~ probe Ba, both being hybridized with the target nucleic ~~acids~~acid (Fa, Sa), thereby obtaining ~~probes~~ a probe having both Aa and Ba as set forth in (Aa+Ba);

(d) binding the first binding molecules of probe Aa to substances capable of being paired up therewith, thereby recovering the ~~probes~~ probe (Aa+Ba);

(e) dissociating the flag ~~sequences~~sequence (D0<sub>j</sub>, D1<sub>k</sub>);

(f) amplifying the flag ~~sequences~~sequence (D0<sub>j</sub>, D1<sub>k</sub>) by PCR, wherein the PCR uses a primer to which a marker substance is bound, and thereby obtaining the flag ~~sequences~~sequence (D0<sub>j</sub>, D1<sub>k</sub>) to which the marker substance is bound; and

(g) detecting or quantifying the marker substance of the flag ~~sequences~~sequence (D0<sub>j</sub>, D1<sub>k</sub>), thereby detecting or quantifying the target nucleic ~~acids~~acid (Fa, Sa).

18. (Cancelled)

19. (Currently amended) The method according to claim 17, wherein step (e) further comprises:

amplifying the dissociated flag ~~sequences~~sequence (D0<sub>j</sub>, D1<sub>k</sub>) by PCR,

wherein the PCR uses a primer to which a second binding molecule is bound, and thereby obtains the flag ~~sequences~~sequence (D0<sub>j</sub>, D1<sub>k</sub>) to which the second binding molecule is bound, and

binding the second binding molecules of the flag ~~sequences~~sequence (D0<sub>j</sub>, D1<sub>k</sub>) to substances capable of being paired up therewith, thereby recovering the flag ~~sequences~~sequence (D0<sub>j</sub>, D1<sub>k</sub>).

20-21. (Cancelled)

22. (Currently amended) The method according to claim 17, wherein, in said step (d), said substance capable of being paired up with the first binding molecules ~~are~~is immobilized on

beads such that the ~~probes~~probe (Aa, Ba) ~~are~~is recovered by binding ~~the probe (Aa, Ba)~~ to the beads via the first binding molecules.

23. (Previously presented) The method according to claim 17, wherein said marker substance is a fluorescent substance such that the target nucleic acids are detected or quantified by quantifying the fluorescent substance.

24. (Cancelled)

25. (Currently amended) The method according to claim 17, wherein each of said flag sequences (D0<sub>j</sub>, D1<sub>k</sub>) ~~are~~is a double stranded ~~sequence~~sequence.

26-33. (Cancelled)